RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form: .

Application Serial Number: **O9/920,137B**
Source: **IFW16**
Date Processed by STIC: **10/1/04**

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT
MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.2 PROGRAM, ACCESSIBLE THROUGH THE U-S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 06/05/04):
   U.S. Patent and Trademark Office, 220 20th Street S., Customer Window, Mail Stop Sequence, Crystal Plaza Two, Lobby, Room 1B03, Arlington, VA 22202

Revised 05/17/04

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: **09/920,137** B

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 ____ Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line. This may occur if your file
Wrapped Aminos was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will
prevent "wrapping."

2 ____ Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 __✓_ Misaligned Amino The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers;
Numbering use space characters, instead.

4 ____ Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please
ensure your subsequent submission is saved in ASCII text.

5 ____ Variable Length Sequence(s) ____ contain n's or Xaa's representing more than one residue. Per Sequence Rules,
each n or Xaa can only represent a single residue. Please present the maximum number of each
residue having variable length and indicate in the <220>-<223> section that some may be missing

6 ____ PatentIn 2.0 A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
"bug" sequences(s) _____. Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to
the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for
Artificial or Unknown sequences.

7 ____ Skipped Sequences Sequence(s) ____ missing. If intentional, please insert the following lines for each skipped sequence
(OLD RULES) (2) INFORMATION FOR SEQ ID NO:X (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION SEQ ID NO X (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES " response to include the skipped sequences

8 ____ Skipped Sequences Sequence(s) ____ missing. If intentional, please insert the following lines for each skipped sequence
(NEW RULES) <210> sequence id number
<400> sequence id number
000

9 ____ Use of n's or Xaa's Use of n's and/or Xaa's have been detected in the Sequence Listing
(NEW RULES) Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents

10 ____ Invalid <213> Per 1.823 of Sequence Rules, the only valid <213> responses are Unknown, Artificial Sequence, or
Response scientific name (Genus/species) <220>-<223> section is required when <213> response is Unknown or
is Artificial Sequence

11 ____ Use of <220> Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or
"Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

12 ____ PatentIn 2.0 Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file,
"bug" resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence
listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 ____ Misuse of n/Xaa "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid

IFW16

```
RAW SEQUENCE LISTING            DATE: 10/01/2004
PATENT APPLICATION: US/09/920,137B    TIME: 10:46:27

Input Set : A:\Cen 0250 SEQ LIST 07-09-01.txt
Output Set: N:\CRF4\10012004\I920137B.raw
```

```
 5 <110> APPLICANT: Giles-Komar, Jill
 6           David Shealy
 7           David Knight
 8           Bernie Scallon
 9           George Heavner
11 <120> TITLE OF INVENTION: ANTI-TNF ANTIBODIES, COMPOSITIONS, METHODS AND USES
13 <130> FILE REFERENCE: CEN0250
C--> 15 <140> CURRENT APPLICATION NUMBER: US/09/920,137B
C--> 15 <141> CURRENT FILING DATE: 2001-08-01
    15 <160> NUMBER OF SEQ ID NOS: 15
    17 <170> SOFTWARE: PatentIn Ver 3.1
```

ERRORED SEQUENCES

```
    19 <210> SEQ ID NO: 1
    20 <211> LENGTH: 5
    21 <212> TYPE: PRT
    22 <213> ORGANISM: Homo sapiens
W--> 23 <400> SEQUENCE: 1
    25 Arg Tyr Thr Met His
E--> 26
    28 <210> SEQ ID NO: 2
    29 <211> LENGTH: 17
    30 <212> TYPE: PRT
    31 <213> ORGANISM: Homo sapiens
W--> 32 <400> SEQUENCE: 2
    34 Val Ile Ser Phe Asp Gly Ser Asn Lys Tyr Tyr Val Asp Ser Val Lys
E--> 35
    37 <210> SEQ ID NO: 3
    38 <211> LENGTH: 10
    39 <212> TYPE: PRT
    40 <213> ORGANISM: Homo sapiens
W--> 41 <400> SEQUENCE: 3
    43 Glu Ala Arg Gly Ser Tyr Ala Phe Asp Ile
E--> 44
    64 <210> SEQ ID NO: 6
    65 <211> LENGTH: 10
    66 <212> TYPE: PRT
    67 <213> ORGANISM: Homo sapiens
W--> 68 <400> SEQUENCE: 6
    70 Gln Gln Arg Ser Asn Trp Pro Pro Phe Thr
E--> 71
```

Handwritten annotations: Does Not Comply / Corrected Diskette Needed / (PJ.1-3) / ← Pls see item #3 on error summary sheet. / ①-Found 16

RAW SEQUENCE LISTING   DATE: 10/01/2004
PATENT APPLICATION: US/09/920,137B   TIME: 10:46:27

Input Set : **A:\Cen 0250 SEQ LIST 07-09-01.txt**
Output Set: **N:\CRF4\10012004\I920137B.raw**

```
      192  <210> SEQ ID NO. 13
      193  <211> LENGTH: (32)  — Found 42
      194  <212> TYPE: DNA
      195  <213> ORGANISM: Homo sapiens
W--> 196  <400> SEQUENCE: 13
E--> 198   ctctcctgca gggccagtca gagtgttagc agctacttag cc
```

32 — 42

VERIFICATION SUMMARY   DATE: 10/01/2004
PATENT APPLICATION: US/09/920,137B   TIME: 10:46:28

Input Set : A:\Cen 0250 SEQ LIST 07-09-01.txt
Output Set: N:\CRF4\10012004\I920137B.raw

```
L:15  M:270 C: Current Application Number differs, Replaced Current Application No
L:15  M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:23  M:283 W: Missing Blank Line separator, <400> field identifier
L:26  M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:1
L:32  M:283 W: Missing Blank Line separator, <400> field identifier
L:35  M:252 E: No. of Seq. differs, <211> LENGTH:Input:17 Found:16 SEQ:2
L:41  M:283 W: Missing Blank Line separator, <400> field identifier
L:44  M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:3
L:50  M:283 W: Missing Blank Line separator, <400> field identifier
L:59  M:283 W: Missing Blank Line separator, <400> field identifier
L:68  M:283 W: Missing Blank Line separator, <400> field identifier
L:71  M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:6
L:77  M:283 W: Missing Blank Line separator, <400> field identifier
L:108 M:283 W: Missing Blank Line separator, <400> field identifier
L:136 M:283 W: Missing Blank Line separator, <400> field identifier
L:172 M:283 W: Missing Blank Line separator, <400> field identifier
L:180 M:283 W: Missing Blank Line separator, <400> field identifier
L:188 M:283 W: Missing Blank Line separator, <400> field identifier
L:196 M:283 W: Missing Blank Line separator, <400> field identifier
L:198 M:254 E: No. of Bases conflict, LENGTH:Input:32 Counted:42 SEQ:13
L:198 M:252 E: No. of Seq. differs, <211> LENGTH:Input:32 Found:42 SEQ:13
L:204 M:283 W: Missing Blank Line separator, <400> field identifier
L:212 M:283 W: Missing Blank Line separator, <400> field identifier
```